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          RAW SEQUENCE LISTING              DATE: 09/27/2001
          PATENT APPLICATION: US/09/825,012  TIME: 14:52:56

               Input Set : A:\Sequence.txt
               Output Set: N:\CRF3\09272001\I825012.raw

   3 <110> APPLICANT: Young, Robert
   5 <120> TITLE OF INVENTION: Compounds for Targeting
   7 <130> FILE REFERENCE: 43191-256808
   9 <140> CURRENT APPLICATION NUMBER: US 09/825,012
  10 <141> CURRENT FILING DATE: 2001-04-03
  12 <150> PRIOR APPLICATION NUMBER: US 60/237,159
  13 <151> PRIOR FILING DATE: 2000-10-02
  15 <150> PRIOR APPLICATION NUMBER: GB 0008049.9
  16 <151> PRIOR FILING DATE: 2000-04-03
  18 <160> NUMBER OF SEQ ID NOS: 102
  20 <170> SOFTWARE: PatentIn version 3.1
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 282
  24 <212> TYPE: PRT
  25 <213> ORGANISM: Homo sapiens
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  34              20                  25                  30
  37 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
  38          35                  40                  45
  41 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
  42      50                  55                  60
  45 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
  46 65                  70                  75                  80
  49 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
  50                  85                  90                  95
  53 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
  54              100                 105                 110
  57 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
  58          115                 120                 125
  61 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
  62      130                 135                 140
  65 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
  66 145                 150                 155                 160
  69 Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
  70                  165                 170                 175
  73 Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
  74              180                 185                 190
  77 Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
  78          195                 200                 205
  81 Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
  82      210                 215                 220
  85 Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
  86 225                 230                 235                 240
  89 Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
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93 Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
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97 Asp His Tyr Pro Val Glu Val Met Leu Lys
98         275           280
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102 <211> LENGTH: 1039
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 2
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109 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag     120
111 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg     180
113 ggggcgctgc tggcactggc ggccctactg caggggggccg tgtccctgaa gatcgcagcc     240
115 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt     300
117 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg     360
119 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac     420
121 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg     480
123 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg     540
125 aacgacacct caaccgaga gccagccatt gtcaggttct ctcccggtt cacagaggtc      600
127 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac     660
129 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg     720
131 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc     780
133 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca     840
135 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgccgtt     900
137 gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg     960
139 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc    1020
141 cacaccagtt gaactgcag                                                  1039
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145 <211> LENGTH: 260
146 <212> TYPE: PRT
147 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 3
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155 Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr
156             20            25             30
159 Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val
160         35            40             45
163 Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His
164     50                55            60
167 Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr
168 65          70            75                80
171 Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr
172             85            90             95
175 Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu
176             100           105            110
179 Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe
180             115           120            125
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```
183 Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
184         130             135             140
187 Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu
188 145             150             155             160
191 Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val
192             165             170             175
195 Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe
196             180             185             190
199 Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His
200         195             200             205
203 Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala
204         210             215             220
207 Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly
208 225             230             235             240
211 Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu
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215 Val Met Leu Lys
216             260
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220 <211> LENGTH: 783
221 <212> TYPE: DNA
222 <213> ORGANISM: Homo sapiens
224 <400> SEQUENCE: 4
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229 agagacagcc acctgactgc cgtggggaag ctgctggaca acctcaatca ggacgcacca   180
231 gacacctatc actacgtggt cagtgagcca ctgggacgga acagctataa ggagcgctac   240
233 ctgttcgtgt acaggcctga ccaggtgtct gcggtggaca gctactacta cgatgatggc   300
235 tgcgagccct gcgggaacga caccttcaac cgagagccag ccattgtcag gttcttctcc   360
237 cggttcacag aggtcaggga gtttgccatt gttcccctgc atgcggcccc gggggacgca   420
239 gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaagagaa atggggcttg   480
241 gaggacgtca tgttgatggg cgacttcaat gcgggctgca gctatgtgag accctcccag   540
243 tggtcatcca tccgcctgtg gacaagcccc accttccagt ggctgatccc cgacagcgct   600
245 gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtggttgc agggatgctg   660
247 ctccgagggg ccgttgttcc cgactcggct cttcccttta acttccaggc tgcctatggc   720
249 ctgagtgacc aactggccca agccatcagt gaccactatc cagtggaggt gatgctgaag   780
251 tga                                                                 783
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255 <211> LENGTH: 161
256 <212> TYPE: PRT
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259 <400> SEQUENCE: 5
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265 Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
266             20              25              30
269 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
270         35              40              45
273 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
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277 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
278 65                    70                    75                    80
281 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
282                   85                    90                    95
285 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
286                   100                   105                   110
289 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
290             115                   120                   125
293 Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
294       130                   135                   140
297 Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
298 145                   150                   155                   160
301 Asp
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305 <210> SEQ ID NO: 6
306 <211> LENGTH: 858
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 6

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313 caggggccg  tgtccctgaa gatcgcagcc ttcaacatcc agacatttgg ggagaccaag     120
315 atgtccaatg ccaccctcgt cagctacatt gtgcagatcc tgagccgcta cgacatcgcc     180
317 ctggtccagg aggtcagaga cagccacctg actccgtgg  ggaagctgct ggacaacctc     240
319 aatcaggacg caccagacac ctatcactac gtggtcagtg agccactggg acggaacagc     300
321 tataaggagc gctacctgtt cgtgtacagg cctgaccagg tgtctgcggt ggacagctac     360
323 tactacgatg atggctgcga gccctgcggg aacgacacct caaccgaga  gccagccatt     420
325 gtcaggttct tctcccggtt cacagaggtc agggagtttg ccattgttcc cctgcatgcg     480
327 gccccggggg acgcagtagc cgagatcgac gctctctatg acgtctacct ggatgtccaa     540
329 gagaaatggg gcttggagga cgtcatgttg atgggcgact tcaatgcggg ctgcagctat     600
331 gtgagaccct cccagtggtc atccatccgc ctgtggacaa gccccacctt ccagtggctg     660
333 atccccgaca gcgctgacac cacagctaca cccacgcact gtgcctatga caggatcgtg     720
335 gttgcaggga tgctgctccg aggggccgtt gttcccgact cggctcttcc ctttaacttc     780
337 caggctgcct atggcctgag tgaccaactg gcccaagcca tcagtgacca ctatccagtg     840
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344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
348 <223> OTHER INFORMATION: Humanised HMFG-1 light chain
350 <400> SEQUENCE: 7

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355 acctgtaagt ccagtcagag cctttttatat agtagcaatc aaaagatcta cttggcctgg     180
357 taccagcaga agccaggtaa ggctccaaag ctgctgatct actgggcatc cactagggaa     240
359 tctggtgtgc caagcagatt cagcggtagc ggtagcggta ccgacttcac cttcaccatc     300
361 agcagcctcc agccagagga catcgccacc tactactgcc agcaatatta tagatatcct     360
363 cggacgttcg gccaagggac caaggtggaa atcaaacgaa ctgtggctgc accatctgtc     420
365 ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg     480
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367 ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa      540
369 tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc      600
371 agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa      660
373 gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg gagagtgttag    720
375 a                                                                      721
378 <210> SEQ ID NO: 8
379 <211> LENGTH: 730
380 <212> TYPE: DNA
381 <213> ORGANISM: Artificial Sequence
383 <220> FEATURE:
384 <223> OTHER INFORMATION: Humanised HMFG-1 light chain
386 <400> SEQUENCE: 8
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391 gtgaccatca cctgtaagtc cagtcagagc cttttatata gtagcaatca aaagatctac      180
393 ttggcctggt accagcagaa gccaggtaag gctccaaagc tgctgatcta ctgggcatcc      240
395 actagggaat ctggtgtgcc aagcagattc agcggtagcg gtagcggtac cgacttcacc      300
397 ttcaccatca gcagcctcca gccagaggac atcgccacct actactgcca gcaatattat      360
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401 ccatctgtct tcatcttccc gccatctgat gagcagttga atctggaac tgcctctgtt       480
403 gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa ggtggataac      540
405 gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc      600
407 tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca caaagtctac      660
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416 <212> TYPE: PRT
417 <213> ORGANISM: Artificial Sequence
419 <220> FEATURE:
420 <223> OTHER INFORMATION: Humanised HMFG-1 light chain
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429                  20                  25                  30
432 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu
433              35                  40                  45
436 Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys
437      50                  55                  60
440 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
441 65                  70                  75                  80
444 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
445                  85                  90                  95
448 Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr
449                  100                 105                 110
452 Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gln Gly Thr Lys
453              115                 120                 125
456 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
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VERIFICATION SUMMARY
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